*Mail*

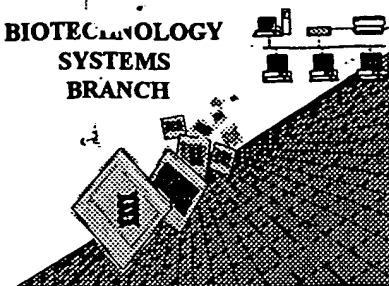# RAW SEQUENCE LISTING
# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/914,220_

Source: _Pu/09_

Date Processed by STIC: _9/14/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1)  INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2)  TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS,  PLEASE CONTACT MARK SPENCER,  703-308-4212.

FOR SEQUENCE RULES INTERPRETATION,  PLEASE CONTACT ROBERT WAX,  703-308-4216.
PATENTIN 2.1 e-mail help:  patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help:  patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE.  SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
### http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING      DATE: 09/14/2001
PATENT APPLICATION: US/09/914,220    TIME: 10:39:35

Input Set : A:\Debelseq.txt
Output Set: N:\CRF3\09142001\I914220.raw

**Does Not Comply
Corrected Diskette Needed**

```
  3 <110> APPLICANT: Schulz Dr., Burkhard
  5 <120> TITLE OF INVENTION: DNA sequence of a protein that is similar to FKBP
  7 <130> FILE REFERENCE: SCU-001 PCT
  9 <140> CURRENT APPLICATION NUMBER: US/09/914,220
 10 <141> CURRENT FILING DATE: 2001-08-22
 12 <150> PRIOR APPLICATION NUMBER: DE 199 07 598.0
 13 <151> PRIOR FILING DATE: 1999-02-22
 15 <160> NUMBER OF SEQ ID NOS: 8
 17 <170> SOFTWARE: PatentIn Ver. 2.1
```

**ERRORED SEQUENCES**

```
309 <210> SEQ ID NO: 7
310 <211> LENGTH: 776
311 <212> TYPE: DNA
312 <213> ORGANISM: Zea mays
314 <400> SEQUENCE: 7
315 tttttttttt ttttccccg tagcaacagt attattacta gcataatcta aatatgaaag 60
316 ctgcaatata caatggcata aaaggcccctt tgagctccag ttgaaagact gtatgaaact 120
317 atggcataat agtgaacaac atcgtataga gttcataaca actaattgat ccggaccggc 180
318 cgacagttct acagaaaatt caacactcct tataatacaa ggttggtcaa ttaggccacc 240
319 agttctacac aatttctgg taaattatcc tactcgttct tccgtttgaa catcccagcc 300
320 agataaagga taaatgacac cagccactgc cagaacacaa cgaggtactt tgccttcttc 360
321 ggtttcgctt caggacttgg cccaaagaga cctttgtaga gctccttctg cttctggtat 420
322 agggcctttn cttgttccgc gagcaaacgg agctcccgaa tgatctcctt gncttctggg 480
323 gagtacttct tcgctttgag gaaatcttcc ctcgctgatt ctgtctggcc aagttcagat 540
324 ttagctttc ctcgcctgaa cagcgctttg acattacttt catcttctgt caaaacaatg 600
325 ctacactgcg caatagcttc atcgaatctc tttagtttga tcaggcatgc ggccatattg 660
326 agatggcatg gattttcac agccaaggcc atgtctctgt acttccaaa taattgaaac 720
327 atgaaatcat ctcccatgta tgcaatcgcc atttcatatt gctgcatggc ctcctc 776
330 <210> SEQ ID NO: 8
331 <211> LENGTH: 168
332 <212> TYPE: PRT
333 <213> ORGANISM: Zea mays
335 <400> SEQUENCE: 8
336 Glu Glu Ala Met Gln Gln Tyr Glu Met Ala Ile Ala Tyr Met Gly Asp
337   1               5                  10                  15
339 Asp Phe Met Phe Gln Leu Phe Gly Lys Tyr Arg Asp Met Ala Leu Ala
340              20                  25                  30
342 Val Lys Asn Pro Cys His Leu Asn Met Ala Ala Cys Leu Ile Lys Leu
343          35                  40                  45
345 Lys Arg Phe Asp Glu Ala Ile Ala Gln Cys Ser Ile Val Leu Thr Glu
346      50                  55                  60
348 Asp Glu Ser Asn Val Lys Ala Leu Phe Arg Arg Gly Lys Ala Lys Ser
349  65                  70                  75                  80
351 Glu Leu Gly Gln Thr Glu Ser Ala Arg Glu Asp Phe Leu Lys Ala Lys
```

RAW SEQUENCE LISTING                    DATE: 09/14/2001
PATENT APPLICATION:   US/09/914,220     TIME: 10:39:35

Input Set : A:\Debelseq.txt
Output Set: N:\CRF3\09142001\I914220.raw

```
        352                   85          90                95
E--> 354 Lys Tyr Ser Pro Glu Xaa Lys Glu Ile Ile Arg Glu Leu Arg Leu Leu
        355               100          105              110
E--> 357 Ala Glu Gln Xaa Lys Ala Leu Tyr Gln Lys Gln Lys Glu Leu Tyr Lys
        358           115          120              125
     360 Gly Leu Phe Gly Pro Ser Pro Glu Ala Lys Pro Lys Lys Ala Lys Tyr
        361     130              135              140
     363 Leu Val Val Phe Trp Gln Trp Leu Val Ser Phe Ile Leu Tyr Leu Ala
        364 145               150              155              160
     366 Gly Met Phe Lys Arg Lys Asn Glu
        367               165
```

*Item 9*

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/914,220 |
|---|---|---|

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1_____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5._____ Variable Length

Sequence(s)_____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10_____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001